

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 07:21:45 ; Search time 6975 Seconds
(without alignments) 4132.347 Million cell updates/sec

Title: US-10-029-345A-109

Sequence: 665
1 MAHEMTGTQVTERIVALLF.....LGKVGSSSSPSSGSMETIEVS 665

Scoring table:

OLIGO	Xgapop 60.0	Xgapext 60.0
	Ygapop 60.0	Ygapext 60.0
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 3470272 segs, 21671516995 residues

Word size: 1419

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-O=/cgn2_1/USPTO.spool/US10029345/runat.23062004.072139.16034/app_query.fasta_1.839
-DB=GenEmbl -OPMT=fastcap -SUFPIX=0.12.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdd -LIST=75
-DOCALLGN=200 -THR SCORE=qual:15 -THR MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10029345.0CGN_1_1.4545.0runat.23062004.072139.16034 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NRG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vtc:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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No matches found

Search completed: June 23, 2004, 09:29:29
Job time : 6975 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 07:21:45 ; Search time 4399 Seconds

(without alignments)
4514.287 Million cell updates/sec

Title: us-10-029-345a-109

Perfect score: 665
Sequence: 1 MAHEMGTQIVTERIVALLE.....LGVGSGSSRSGSMELIEVS 665

Scoring table:

OLIGO	Xgapop 60.0	Xgapext 60.0
Ygapop 60.0	Ygapext 60.0	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 27513289 seqs, 14931090276 residues

Word size: 1419

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-O=/cgn2_1/USPTO.spool/US10029345/runat_23062004_072140_16043/app_query.fasta_1.839
-DB=EST -CPMT=fastcap -SUFFIX=0112.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=1 -MATRIX=01igo -TRANS=human40.cdi -LIST=75
-DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10029345 @CGN_1_1_3437 @runat_23062004_072140_16043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_g88_hum: *
18: em_g88_iny: *
19: em_g88_pln: *
20: em_g88_vic: *
21: em_g88_fun: *
22: em_g88_mam: *
23: em_g88_mus: *
24: em_g88_pro: *
25: em_g88_rtd: *
26: em_g88_phg: *
27: em_g88_vrl: *
28: gb_g88l: *

29: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: June 23, 2004, 10:42:56
Job time : 4399 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 07:21:45 ; Search time 670 Seconds

(without alignments)
4216.495 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665
Sequence: 1 MAHEMIGTQVTERLVALL.....LGKVGSGSFSGSMIEIVS 665

Scoring table:

OLIGO	Xgapop 60.0	Xgapext 60.0
	Ygapop 60.0	Ygapext 60.0
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 337863 segs, 212409041 residues

Word size: 1419

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=x1h
-O=/cgn2_1/USPTO.spool/US10029345/runat_23062004_072139_16024/app_query.fasta_1.839
-DB=N_Geneseq_29Jan04 -CPMT=fastap -SUFFIX=0112.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0190 -TRANS=human40.cdt
-LIST=75 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10029345_QCGN_1_1_470_@runat_23062004_072139_16024 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	ID	Description
No.	Score				

No matches found

Search completed: June 23, 2004, 07:33:06
Job time : 670 secs

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OM protein - nucleic search, using frame_blue_p2n model

Run on: June 23, 2004, 07:21:50 ; Search time 1544 Seconds
(without alignments)
1973.073 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 665
Sequence: 1 MAHEMIGTQVTERLVALLE.....LGKVGSSQSFSGSMETREVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Word size: 1419

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=x1h
-O=/cgnt1/USPTO.spool/US10029345/runat_23062004_072141_16083/app_query.fasta_1.839
-DB=Published_Applications_NA -QFMT=fastlap -SUFFIX=ol12.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=ol1go
-TRANS=numan40.cdi -LIST=75 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1419
-ALIGN=50 -MODE=LOCAL -OUTFMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10029345_@CGN_1_1_485_@runat_23062004_072141_16083
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published_Applications_NA.*
1: /cgnt2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgnt2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgnt2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgnt2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgnt2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgnt2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgnt2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgnt2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgnt2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgnt2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgnt2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgnt2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgnt2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgnt2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgnt2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgnt2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgnt2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgnt2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgnt2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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No matches found

Search completed: June 23, 2004, 11:11:03
Job time : 1545 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 07:21:50 ; Search time 125 Seconds
(without alignments)
2952.339 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 665
Sequence: 1 MAHEMIGTQVTERLVALL.....LGRVSGSSSFSGSMETIEVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 1419

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10029345/runat_23062004_072140_16059/app_query.fasta_1.839
-DB=Issued_Patents_NA -OPMT=fastcap -SUFFIX=ol12.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -EMD=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=75 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1419 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029345 @CGN 1_1_69@runat_23062004_072140_16059 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEIOUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -Ygapop=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:

- 1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description

No matches found				

Search completed: June 23, 2004, 10:45:09
Job time : 125 secs

11.15 Page Blank (uspio)